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P.5

RAW SEQUENCE LISTING   DATE: 12/14/2001
PATENT APPLICATION: US/10/005,344   TIME: 10:09:38

Input Set : A:\ISPH622_Sequence Listing.txt
Output Set: N:\CRF3\12142001\I005344.raw

ENTERED

```
 4 <110> APPLICANT: Loren J. Miraglia
 5         Pamela Nero
 6         Mark J. Graham
 7         Brett P. Monia
 8         Erich Koller
 9         MingYi Chiang
10         Mano Manoharan
12 <120> TITLE OF INVENTION: Antisense Modulation of mdm2 expression.
14 <130> FILE REFERENCE: ISPH-0622
16 <140> CURRENT APPLICATION NUMBER: US/10/005,344
17 <141> CURRENT FILING DATE: 2001-12-04
19 <150> PRIOR APPLICATION NUMBER: US 09/048,810
20 <151> PRIOR FILING DATE: 1998-03-26
22 <150> PRIOR APPLICATION NUMBER: US 09/280,805
23 <151> PRIOR FILING DATE: 1999-03-26
25 <160> NUMBER OF SEQ ID NOS: 379
27 <170> SOFTWARE: FastSEQ for Windows Version 4.0
29 <210> SEQ ID NO: 1
30 <211> LENGTH: 2372
31 <212> TYPE: DNA
32 <213> ORGANISM: Homo sapiens
34 <220> FEATURE:
35 <221> NAME/KEY: CDS
36 <222> LOCATION: (312)...(1787)
38 <400> SEQUENCE: 1
39 gcaccgcgcg agcttggctg cttctggggc ctgtgtggcc ctgtgtgtcg gaaagatgga  60
40 gcaagaagcc gagcccgagg ggcggccgcg acccctctga ccgagatcct gctgctttcg 120
41 cagccaggag caccgtccct ccccggatta gtgcgtacga gcgcccagtg ccctggcccg 180
42 gagagtggaa tgatccccga ggcccagggc gtcgtgcttc cgcagtagtc agtccccgtg 240
43 aaggaaactg gggagtcttg agggacccccc gactccaagc gcgaaaccc cggatggtga 300
44 ggagcaggca a atg tgc aat acc aac atg tct gta cct act gat ggt gct 350
45                Met Cys Asn Thr Asn Met Ser Val Pro Thr Asp Gly Ala
46                 1               5                   10
48 gta acc acc tca cag att cca gct tcg gaa caa gag acc ctg gtt aga 398
49 Val Thr Thr Ser Gln Ile Pro Ala Ser Glu Gln Glu Thr Leu Val Arg
50      15                  20                  25
52 cca aag cca ttg ctt ttg aag tta tta aag tct gtt ggt gca caa aaa 446
53 Pro Lys Pro Leu Leu Leu Lys Leu Leu Lys Ser Val Gly Ala Gln Lys
54  30              35                  40                  45
56 gac act tat act atg aaa gag gtt ctt ttt tat ctt ggc cag tat att 494
57 Asp Thr Tyr Thr Met Lys Glu Val Leu Phe Tyr Leu Gly Gln Tyr Ile
58              50                  55                  60
60 atg act aaa cga tta tat gat gag aag caa caa cat att gta tat tgt 542
61 Met Thr Lys Arg Leu Tyr Asp Glu Lys Gln Gln His Ile Val Tyr Cys
62          65                  70                  75
64 tca aat gat ctt cta gga gat ttg ttt ggc gtg cca agc ttc tct gtg 590
65 Ser Asn Asp Leu Leu Gly Asp Leu Phe Gly Val Pro Ser Phe Ser Val
```

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66          80                    85                        90
68 aaa gag cac agg aaa ata tat acc atg atc tac agg aac ttg gta gta    638
69 Lys Glu His Arg Lys Ile Tyr Thr Met Ile Tyr Arg Asn Leu Val Val
70       95                  100                      105
72 gtc aat cag cag gaa tca tcg gac tca ggt aca tct gtg agt gag aac    686
73 Val Asn Gln Gln Glu Ser Ser Asp Ser Gly Thr Ser Val Ser Glu Asn
74 110                      115                    120                 125
76 agg tgt cac ctt gaa ggt ggg agt gat caa aag gac ctt gta caa gag    734
77 Arg Cys His Leu Glu Gly Gly Ser Asp Gln Lys Asp Leu Val Gln Glu
78             130                      135                    140
80 ctt cag gaa gag aaa cct tca tct tca cat ttg gtt tct aga cca tct    782
81 Leu Gln Glu Glu Lys Pro Ser Ser Ser His Leu Val Ser Arg Pro Ser
82             145                    150                    155
84 acc tca tct aga agg aga gca att agt gag aca gaa gaa aat tca gat    830
85 Thr Ser Ser Arg Arg Arg Ala Ile Ser Glu Thr Glu Glu Asn Ser Asp
86             160                    165                    170
88 gaa tta tct ggt gaa cga caa aga aaa cgc cac aaa tct gat agt att    878
89 Glu Leu Ser Gly Glu Arg Gln Arg Lys Arg His Lys Ser Asp Ser Ile
90       175                  180                      185
92 tcc ctt tcc ttt gat gaa agc ctg gct ctg tgt gta ata agg gag ata    926
93 Ser Leu Ser Phe Asp Glu Ser Leu Ala Leu Cys Val Ile Arg Glu Ile
94 190                      195                    200                 205
96 tgt tgt gaa aga agc agt agc agt gaa tct aca ggg acg cca tcg aat    974
97 Cys Cys Glu Arg Ser Ser Ser Ser Glu Ser Thr Gly Thr Pro Ser Asn
98             210                    215                    220
100 ccg gat ctt gat gct ggt gta agt gaa cat tca ggt gat tgg ttg gat   1022
101 Pro Asp Leu Asp Ala Gly Val Ser Glu His Ser Gly Asp Trp Leu Asp
102             225                    230                    235
104 cag gat tca gtt tca gat cag ttt agt gta gaa ttt gaa gtt gaa tct   1070
105 Gln Asp Ser Val Ser Asp Gln Phe Ser Val Glu Phe Glu Val Glu Ser
106             240                    245                    250
108 ctc gac tca gaa gat tat agc ctt agt gaa gaa gga caa gaa ctc tca   1118
109 Leu Asp Ser Glu Asp Tyr Ser Leu Ser Glu Glu Gly Gln Glu Leu Ser
110       255                  260                      265
112 gat gaa gat gat gag gta tat caa gtt act gtg tat cag gca ggg gag   1166
113 Asp Glu Asp Asp Glu Val Tyr Gln Val Thr Val Tyr Gln Ala Gly Glu
114 270                      275                    280                 285
116 agt gat aca gat tca ttt gaa gaa gat cct gaa att tcc tta gct gac   1214
117 Ser Asp Thr Asp Ser Phe Glu Glu Asp Pro Glu Ile Ser Leu Ala Asp
118             290                    295                    300
120 tat tgg aaa tgc act tca tgc aat gaa atg aat ccc ccc ctt cca tca   1262
121 Tyr Trp Lys Cys Thr Ser Cys Asn Glu Met Asn Pro Pro Leu Pro Ser
122             305                    310                    315
124 cat tgc aac aga tgt tgg gcc ctt cgt gag aat tgg ctt cct gaa gat   1310
125 His Cys Asn Arg Cys Trp Ala Leu Arg Glu Asn Trp Leu Pro Glu Asp
126             320                    325                    330
128 aaa ggg aaa gat aaa ggg gaa atc tct gag aaa gcc aaa ctg gaa aac   1358
129 Lys Gly Lys Asp Lys Gly Glu Ile Ser Glu Lys Ala Lys Leu Glu Asn
130       335                  340                      345
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132 tca aca caa gct gaa gag ggc ttt gat gtt cct gat tgt aaa aaa act  1406
133 Ser Thr Gln Ala Glu Glu Gly Phe Asp Val Pro Asp Cys Lys Lys Thr
134 350                 355                 360                 365
136 ata gtg aat gat tcc aga gag tca tgt gtt gag gaa aat gat gat aaa  1454
137 Ile Val Asn Asp Ser Arg Glu Ser Cys Val Glu Glu Asn Asp Asp Lys
138                 370                 375                 380
140 att aca caa gct tca caa tca caa gaa agt gaa gac tat tct cag cca  1502
141 Ile Thr Gln Ala Ser Gln Ser Gln Glu Ser Glu Asp Tyr Ser Gln Pro
142             385                 390                 395
144 tca act tct agt agc att att tat agc agc caa gaa gat gtg aaa gag  1550
145 Ser Thr Ser Ser Ser Ile Ile Tyr Ser Ser Gln Glu Asp Val Lys Glu
146             400                 405                 410
148 ttt gaa agg gaa gaa acc caa gac aaa gaa gag agt gtg gaa tct agt  1598
149 Phe Glu Arg Glu Glu Thr Gln Asp Lys Glu Glu Ser Val Glu Ser Ser
150     415                 420                 425
152 ttg ccc ctt aat gcc att gaa cct tgt gtg att tgt caa ggt cga cct  1646
153 Leu Pro Leu Asn Ala Ile Glu Pro Cys Val Ile Cys Gln Gly Arg Pro
154 430                 435                 440                 445
156 aaa aat ggt tgc att gtc cat ggc aaa aca gga cat ctt atg gcc tgc  1694
157 Lys Asn Gly Cys Ile Val His Gly Lys Thr Gly His Leu Met Ala Cys
158                 450                 455                 460
160 ttt aca tgt gca aag aag cta aag aaa agg aat aag ccc tgc cca gta  1742
161 Phe Thr Cys Ala Lys Lys Leu Lys Lys Arg Asn Lys Pro Cys Pro Val
162             465                 470                 475
164 tgt aga caa cca att caa atg att gtg cta act tat ttc ccc tag      1787
165 Cys Arg Gln Pro Ile Gln Met Ile Val Leu Thr Tyr Phe Pro *
166             480                 485                 490
168 ttgacctgtc tataagagaa ttatatattt ctaactatat aaccctagga atttagacaa 1847
169 cctgaaattt attcacatat atcaaagtga gaaaatgcct caattcacat agatttcttc 1907
170 tctttagtat aattgaccta ctttggtagt ggaatagtga atacttacta taatttgact 1967
171 tgaatatgta gctcatcctt tacaccaact cctaatttta aataatttct actctgtctt 2027
172 aaatgagaag tacttggttt ttttttctt aaatatgtat atgacattta aatgtaactt 2087
173 attatttttt ttgagaccga gtcttgctct gttacccagg ctggagtgca gtgggtgatc 2147
174 ttggctcact gcaagctctg ccctccccgg gttcgcacca ttctcctgcc tcagcctccc 2207
175 aattagcttg gcctacagtc atctgccacc acacctggct aatttttgt actttagta   2267
176 gagacagggt ttcaccgtgt tagccaggat ggtctcgatc tcctgacctc gtgatccgcc 2327
177 cacctcggcc tcccaaagtg ctgggattac aggcatgagc caccg                 2372
179 <210> SEQ ID NO: 2
180 <211> LENGTH: 500
181 <212> TYPE: DNA
182 <213> ORGANISM: Homo sapiens
184 <220> FEATURE:
185 <221> NAME/KEY: misc_signal
186 <222> LOCATION: (138)...(157)
187 <223> OTHER INFORMATION: p53 response element RE1
189 <221> NAME/KEY: misc_signal
190 <222> LOCATION: (176)...(195)
191 <223> OTHER INFORMATION: p53 response element RE2
193 <221> NAME/KEY: exon
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RAW SEQUENCE LISTING   DATE: 12/14/2001
PATENT APPLICATION: US/10/005,344   TIME: 10:09:38

Input Set : A:\ISPH622_Sequence Listing.txt
Output Set: N:\CRF3\12142001\I005344.raw

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194 <222> LOCATION: (231)...(301)
195 <223> OTHER INFORMATION: Exon 2
197 <221> NAME/KEY: intron
198 <222> LOCATION: (302)...(422)
199 <223> OTHER INFORMATION: Intron 2
201 <400> SEQUENCE: 2
202 ggctgcgggc ccctgcggcg cgggaggtcc ggatgatcgc aggtgcctgt cgggtcacta 60
203 gtgtgaacgc tgcgcgtagt ctgggcggga ttgggccggt tcagtgggca ggttgactca 120
204 gcttttcctc ttgagctggt caagttcaga cacgttccga aactgcagta aaaggagtta 180
205 agtcctgact tgtctccagc tggggctatt taaaccatgc attttcccag ctgtgttcag 240
206 tggcgattgg agggtagacc tgtgggcacg gacgcacgcc actttttctc tgctgatcca 300
207 ggtaagcacc gacttgcttg tagctttagt tttaactgtt gtttatgttc tttatatatg 360
208 atgtattttc cacagatgtt tcatgatttc cagttttcat cgtgtctttt ttttccttgt 420
209 aggcaaatgt gcaataccaa catgtctgta cctactgatg gggctgtaac caccccacag 480
210 attccagctt cggaacaaga                                          500
212 <210> SEQ ID NO: 3
213 <211> LENGTH: 20
214 <212> TYPE: DNA
215 <213> ORGANISM: Artificial Sequence
217 <220> FEATURE:
218 <223> OTHER INFORMATION: Antisense Oligonucleotide
220 <400> SEQUENCE: 3
221 cagccaagct cgcgcggtgc                                           20
223 <210> SEQ ID NO: 4
224 <211> LENGTH: 20
225 <212> TYPE: DNA
226 <213> ORGANISM: Artificial Sequence
228 <220> FEATURE:
229 <223> OTHER INFORMATION: Antisense Oligonucleotide
231 <400> SEQUENCE: 4
232 tctttccgac acacagggcc                                           20
234 <210> SEQ ID NO: 5
235 <211> LENGTH: 20
236 <212> TYPE: DNA
237 <213> ORGANISM: Artificial Sequence
239 <220> FEATURE:
240 <223> OTHER INFORMATION: Antisense Oligonucleotide
242 <400> SEQUENCE: 5
243 cagcaggatc tcggtcagag                                           20
245 <210> SEQ ID NO: 6
246 <211> LENGTH: 20
247 <212> TYPE: DNA
248 <213> ORGANISM: Artificial Sequence
250 <220> FEATURE:
251 <223> OTHER INFORMATION: Antisense Oligonucleotide
253 <400> SEQUENCE: 6
254 gggcgctcgt acgcactaat                                           20
256 <210> SEQ ID NO: 7
257 <211> LENGTH: 20
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258 <212> TYPE: DNA
259 <213> ORGANISM: Artificial Sequence
261 <220> FEATURE:
262 <223> OTHER INFORMATION: Antisense Oligonucleotide
264 <400> SEQUENCE: 7
265 tcggggatca ttccactctc                                    20
267 <210> SEQ ID NO: 8
268 <211> LENGTH: 20
269 <212> TYPE: DNA
270 <213> ORGANISM: Artificial Sequence
272 <220> FEATURE:
273 <223> OTHER INFORMATION: Antisense Oligonucleotide
275 <400> SEQUENCE: 8
276 cggggttttc gcgcttggag                                    20
278 <210> SEQ ID NO: 9
279 <211> LENGTH: 20
280 <212> TYPE: DNA
281 <213> ORGANISM: Artificial Sequence
283 <220> FEATURE:
284 <223> OTHER INFORMATION: Antisense Oligonucleotide
286 <400> SEQUENCE: 9
287 catttgcctg ctcctcacca                                    20
289 <210> SEQ ID NO: 10
290 <211> LENGTH: 20
291 <212> TYPE: DNA
292 <213> ORGANISM: Artificial Sequence
294 <220> FEATURE:
295 <223> OTHER INFORMATION: Antisense Oligonucleotide
297 <400> SEQUENCE: 10
298 gtattgcaca tttgcctgct                                    20
300 <210> SEQ ID NO: 11
301 <211> LENGTH: 20
302 <212> TYPE: DNA
303 <213> ORGANISM: Artificial Sequence
305 <220> FEATURE:
306 <223> OTHER INFORMATION: Antisense Oligonucleotide
308 <400> SEQUENCE: 11
309 agcaccatca gtaggtacag                                    20
311 <210> SEQ ID NO: 12
312 <211> LENGTH: 20
313 <212> TYPE: DNA
314 <213> ORGANISM: Artificial Sequence
316 <220> FEATURE:
317 <223> OTHER INFORMATION: Antisense Oligonucleotide
319 <400> SEQUENCE: 12
320 ctaccaagtt cctgtagatc                                    20
322 <210> SEQ ID NO: 13
323 <211> LENGTH: 20
324 <212> TYPE: DNA
```

Use of n and / or Xaa has been detected in the
Sequence Listing. Review the Sequence Listing
to ensure a corresponding explanation is present
in the <220> to <223> fields of each sequence
using n or Xaa.

VERIFICATION SUMMARY   DATE: 12/14/2001
PATENT APPLICATION: **US/10/005,344**   TIME: 10:09:39

Input Set : **A:\ISPH622_Sequence Listing.txt**
Output Set: **N:\CRF3\12142001\I005344.raw**

```
L:16   M:270 C: Current Application Number differs, Replaced Application Number
L:17   M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:4424 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:370
L:4425 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:370
L:4536 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:3
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